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'OBI' IS DEFAULT SEARCH FIELD FOR 'HCAPLUS' FILE

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L1 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:539911 HCAPLUS
DN 137:90576
ED Entered STN: 19 Jul 2002
TI Stable isotope, site-specific mass tagging for protein identification
IN Chen, Xian
PA The Regents of the University of California, USA
SO PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N
CC 9-5 (Biochemical Methods)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002055989	A2	20020718	WO 2002-US538	20020111
	WO 2002055989	A3	20021128		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2002146743	A1	20021010	US 2002-43965	20020111 <--
PRAI	US 2001-261716P	P	20010112		
AB	Proteolytic peptide mass mapping as measured by mass spectrometry provides an important method for the identification of proteins, which are usually identified by matching the measured and calculated m/z values of the proteolytic peptides. A unique identification is, however, heavily				

dependent upon the mass accuracy and sequence coverage of the fragment ions generated by peptide ionization. The present invention describes a method for increasing the specificity, accuracy and efficiency of the assignments of particular proteolytic peptides and consequent protein identification, by the incorporation of selected amino acid residue(s) enriched with stable isotope(s) into the protein sequence without the need for ultrahigh instrumental accuracy. Selected amino acids(s) are labeled. With $^{13}\text{C}/^{15}\text{N}/^{2}\text{H}$ and incorporated into proteins in a sequence-specific manner during cell culturing. Each of these labeled amino acids carries a defined mass change encoded in its monoisotopic distribution pattern. Through their characteristic patterns, the peptides with mass tag(s) can be readily distinguished from other peptides in mass spectra. The present method of identifying unique proteins can also be extended to protein complexes and will significantly increase data search specificity, efficiency and accuracy for protein identifications.

ST stable isotope mass tagging protein
 IT Mass spectra
 (Delayed-extraction; stable isotope, site-specific mass tagging for protein identification)
 IT Mass spectra
 (Postsource decay fragment ion; stable isotope, site-specific mass tagging for protein identification)
 IT Peptides, analysis
 RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (UBL1; stable isotope, site-specific mass tagging for protein identification)
 IT Proteins
 RL: ANT (Analyte); ANST (Analytical study)
 (complexes; stable isotope, site-specific mass tagging for protein identification)
 IT Mass spectrometers
 (electrospray-ionization; stable isotope, site-specific mass tagging for protein identification)
 IT Gene
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (expression; stable isotope, site-specific mass tagging for protein identification)
 IT Amino acids, uses
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (labeled; stable isotope, site-specific mass tagging for protein identification)
 IT Gene
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (lesions; stable isotope, site-specific mass tagging for protein identification)
 IT Time-of-flight mass spectrometers
 (matrix-assisted laser desorption/ionization; stable isotope, site-specific mass tagging for protein identification)
 IT Information systems
 (searching; stable isotope, site-specific mass tagging for protein identification)
 IT Cell
 Composition
 Digestion, chemical
 Dilution
 Escherichia coli
 Ionization
 Ions
 Isotope indicators

Labels
Liquid chromatography
Mass
Mass spectra
Mass spectrometers
Mass spectrometry
Mathematical methods
Mixtures
Protein degradation
Protein sequences
Separation
 (stable isotope, site-specific mass tagging for protein identification)
IT Peptides, analysis
Proteins
RL: ANT (Analyte); ANST (Analytical study)
 (stable isotope, site-specific mass tagging for protein identification)
IT Proteome
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (stable isotope, site-specific mass tagging for protein identification)
IT Gel electrophoresis
 (two-dimensional; stable isotope, site-specific mass tagging for protein identification)
IT 4896-75-7, Glycine-2,2-d2 7782-39-0, Hydrogen-2, uses 14390-96-6,
Nitrogen-15, uses 14762-74-4, Carbon-13, uses 349086-43-7,
L-Methionine-d3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (stable isotope, site-specific mass tagging for protein identification)
IT 26112-89-0, Isopropylthiogalactoside
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
 (stable isotope, site-specific mass tagging for protein identification)
IT 9001-92-7, Protease 9002-07-7, Trypsin
RL: CAT (Catalyst use); USES (Uses)
 (stable isotope, site-specific mass tagging for protein identification)

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